



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

- (i) APPLICANT: Gonzalez, Frank J.  
Fernandez-Salguero, Pedro
- (ii) TITLE OF INVENTION: Methods and Compositions for Detecting  
Dihydropyrimidine Dehydrogenase Splicing Mutations
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Townsend and Townsend and Crew LLP  
(B) STREET: Two Embarcadero Center, Eighth Floor  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/308,080  
(B) FILING DATE: 28-OCT-1999  
(C) CLASSIFICATION:
- a<sup>10</sup> (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/013,835  
(B) FILING DATE: 20-MAR-1996
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: WO PCT/US97/04269  
(B) FILING DATE: 19-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Weber, Kenneth A.  
(B) REGISTRATION NUMBER: 31,677  
(C) REFERENCE/DOCKET NUMBER: 015280-271100US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (415) 576-0200  
(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 861 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 269..433  
(D) OTHER INFORMATION: /note= "dihydropyrimidine dehydrogenase (DPD) gene region of splicing mutant mRNA encoding amino acids 581-635"

(ix) FEATURE:

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(A) NAME/KEY: mutation
(B) LOCATION: replace(434, "a")
(D) OTHER INFORMATION: /note= "G -> A mutation at 3' donor
                        splice junction consensus sequence
                        leading to loss of exon in DPD mRNA
                        and DPD deficiency"
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGTTAATGAA	GATAAATATT	TTTGTTTTTT	CGCTGTTCTA	AACCTAGGGT	TACAAGAAGT		60
AATTTATCTG	GAGCTAACAA	ATACTTTATT	TTACCTTTTT	ATTTGCAAGT	AGTTTATGTT		120
CAATTCTAAT	TTAATGTATA	TTAAAAATTC	CTCTGCAAAT	ATGTGAGGAG	GGACCTCATA		180
AAATATTGTC	ATATGGAAAT	GAGCAGATAA	TAAAGATTAT	AGCTTTTCTT	TGTCAAAAGG		240
AGACTCAATA	TCTTTACTCT	TTCATGAG	GAC ATT GTG ACA AAT GTT TCC CCC				292
			Asp Ile Val Thr Asn Val Ser Pro				
			1 5				
ATA ATC ATC CGG GGA ACC ACC TCT GGC CCC ATG TAT GGC CCT GGA CAA							340
Ile Ile Ile Arg Gly Thr Thr Ser Gly Pro Met Tyr Gly Pro Gly Gln							
10 15 20							
AGC TCC TTT CTG AAT ATT GAG CTC ATC AGT GAG AAA ACG GCT GCA TAT							388
Ser Ser Phe Leu Asn Ile Glu Leu Ile Ser Glu Lys Thr Ala Ala Tyr							
25 30 35 40							
TGG TGT CAA AGT GTC ACT GAA CTA AAG GCT GAC TTC CCA GAC AAC							433
Trp Cys Gln Ser Val Thr Glu Leu Lys Ala Asp Phe Pro Asp Asn							
45 50 55							
GTAAGTGTGA	TAAAAATCTA	AAACAAGAGA	ATTGGCATAA	GTTGGTGAAT	GTTTATTTAA		493
ACATCCAATT	CATAGGCTTA	TAAATATTAA	TGTGTATATT	TTATCAACGA	ATCTGCCAGT		553
TGCTTTGCTG	ATGCATAGAA	AGATAAAAAA	GAAAGAAAAG	CTCAAGAACT	CATAAAAACC		613
CACACAATGT	GAAGCTCTGT	TATAAATGGG	TGCCATGTAA	GATGGAAGAA	GTATCTACAT		673
AAGCAGAAGG	AAGAGAAATG	AAATACTCAT	TTTATTGAGT	TGGCCCCCAC	TGTATGTGGC		733
TGGTATTTAT	GAAGGTGATG	ACCCAGGAAG	AAATTGTAAA	CTATAAACCA	CTCCAAATAT		793
AAACCCGAGG	CAGAAGCAGC	ATATCTCCTA	TGAAGCCTGT	ATTTACTCAG	TGGGAAATAA		853
TTTATTAA							861

(2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ile Val Thr Asn Val Ser Pro Ile Ile Ile Arg Gly Thr Thr Ser  
 1                      5                      10                      15

Gly Pro Met Tyr Gly Pro Gly Gln Ser Ser Phe Leu Asn Ile Glu Leu  
                     20                      25                      30

Ile Ser Glu Lys Thr Ala Ala Tyr Trp Cys Gln Ser Val Thr Glu Leu  
                     35                      40                      45

Lys Ala Asp Phe Pro Asp Asn  
                     50                      55

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "primer DELF1 (forward)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGCAAATATG TGAGGAGGGA CC

22

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "primer DELR1 (reverse)"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCAAAGCA ACTGGCAGAT TC

22

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "primer DPD15F (forward)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTGTGACAAA TGTTTCCC

18

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "primer DPD15R (reverse)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTCAGCCTT TAGTTCAGTG ACAC

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 856 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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TGTTAATGAA GATAAATATT TTTATTTTGG CGCTATTCTA AACCTAGAGT TACAAGAAGT 60  
 AATTTATCTG GAGCTAACAA ATACTTTATT TTACCTTTTT ATTTGCAAGT AGTTTATGTT 120  
 CAATTCTAAT TTAATGTATA TTAAAAATTC CTCTGCAAAT ATGTGAGGAG GGACCTCATA 180  
 AAATATTGTC ATATGGAGAT GAGCAGATAA TAAAGATTAT AGCTTTTCTT TGTCAAAGG 240  
 AGACTCAATA TCTTTACTCT TTCATCAGGA CATTGTGACA AATGTTTCCC CCATAATCAT 300  
 CCGGGGAACC ACCTCTGGCC CCATGTATGG CCCTGGACAA AGCTCCTTTC TGAATATTGA 360  
 GCTCATCAGT GAGAAAACGG CTGCATATTG GTGTCAAAGT GTCACTGAAC TAAAGGCTGA 420  
 CTTCCCAGAC AACGTAAGTG TGATAAAAAT CTAAAACAAG AGAATTGGCA TAAGTTGGTG 480  
 AATGTTTATT TAAACATCCA ATTCATAGGC TTATAAATAT TAATGTGTAT ATTTTATCAA 540  
 AGAATCTGCC AGTTGCTTTG CTGATGCATA GAAAGATAAA AAAGAAAGAA AAGCTCAAGA 600  
 ACTCATAAAA ACCCACACAA TGTGAAGCTC GTTATAAATG GGTGCCATGT AAGATGGAAG 660  
 AAGTATCTAC ATAAGCAGAA GGAAGAGAAA TGAAATACTC AATTTATTGA GTTGGCCCCC 720  
 ACTGTATGTG GCTGGCATTG ATGAAGGTGA TGACCCAGGA AGAAATTGTC ACCTATAAAT 780  
 CATCCAAATA TCCCAGAGCA GAAGCAGCAT CTCTCCTATG AAGTCTGTAT TTATTTTCAGC 840  
 GGGAAATAAT TTATTA 856

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